

**Amendments to the Claims:**

The following listing of claims will replace all prior versions, and listings, of claims in the application:

1–17. (Cancelled)

18. (New) A method, comprising:

- a) providing a sample comprising a nucleic acid fraction;
- b) amplifying the nucleic acid fraction;
- c) contacting the nucleic acid fraction with a combination of

oligonucleotides respectively comprising the sequences set forth in SEQ ID NOs:1–232 and 242–261, or full-length complementary sequences thereof; and

d) detecting formation or non-formation of a hybridization complex between the nucleic acid fraction and the combination of oligonucleotides.

19. (New) The method of claim 18, wherein amplifying the nucleic acid fraction is performed with a primer comprising the sequence set forth in a member selected from the group consisting of SEQ ID NOs:240, 241, and 272–276, and the full-length complementary sequences thereof.

20. (New) The method of claim 18, wherein amplifying the nucleic acid fraction is performed with at least one pair of primers selected from the following pairs of primers:

a primer comprising the sequence set forth in SEQ ID NO:240 or the full-length complementary sequence thereof, and a primer comprising the sequence set forth in SEQ ID NO:241 or the full-length complementary sequence thereof;

a primer comprising the sequence set forth in SEQ ID NO:272 or the full-length complementary sequence thereof and a primer comprising the sequence set forth in SEQ ID NO:273 or the full-length complementary sequence thereof; and

a primer comprising the sequence set forth in SEQ ID NO:274 or the full-length complementary sequence thereof, and a primer comprising the sequence set forth in SEQ ID NO:275 or the full-length complementary sequence thereof.

21. (New) The method of claim 18, further comprising:

determining whether the sample contains a nucleic acid fraction from any organism belonging to a taxonomic group listed in field <213> of SEQ ID NOS:1–232 and 242–261.

22. (New) The method of claim 21, further comprising:

determining which taxonomic group listed in field <213> of SEQ ID NOS:1–232 and 242–261 a nucleic acid fraction from the sample belongs to if the nucleic acid fraction is determined to be from a taxonomic group listed in field <213> of SEQ ID NOS:1–232 and 242–261.

23. (New) The method of claim 18, further comprising:

determining whether the sample does not contain a nucleic acid fraction from one or more predetermined taxonomic group selected from the taxonomic groups listed in field <213> of SEQ ID NOS:1–232 and 242–261.

24. (New) The method of claim 18, further comprising:

determining whether the sample contains a nucleic acid fraction from one or more predetermined taxonomic group selected from the taxonomic groups listed in field <213> of SEQ ID NOS:1–232 and 242–261.

25. (New) The method of claim 18, further comprising:

determining which taxonomic groups listed in field <213> of SEQ ID NOS:1–232 and 242–261 are absent from the sample.

26. (New) The method of claim 18, wherein the sample is selected from the group consisting of foods, cosmetics, and pharmaceuticals.

27. (New) The method of claim 18, wherein the combination of oligonucleotides is arranged and attached in a predetermined manner to a biochip comprising a solid support.

28. (Withdrawn - New) A combination of oligonucleotides respectively comprising the sequences set forth in SEQ ID NOs:1–232 and 242–261, or full-length complementary sequences thereof.

29. (Withdrawn - New) A biochip, comprising:  
a solid support; and  
a combination of oligonucleotides respectively comprising the sequences set forth in SEQ ID NOs:1–232 and 242–261, or full-length complementary sequences thereof, wherein the combination of oligonucleotides is arranged and attached in a predetermined manner to the solid support.